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Amino Acid Sequence of hPygo2

MAASAPPDKLEGGGPAPPPAPPSTGRKQGKAGLQMKSP**EKK**
RRKSNTQGPAYSHLTEFAPPPTMVDHLVASNPFEDDFGAPKVG
VAAPPFLGSPVPFGGFRVQGGMAGQVPPGYSTGGGGPQPLRRQ
PPPFPNPMGPAFNMPPQGPGYPPPGNMNFPSQPFNQPLGQNFS
PPSGQMMPGPVGGFGPMISPTMGQPPRAELGPPSLSQRFAQPGA
PFGPSPLQRPGQGLPSLPPNTSPFPGPDPGFPPGGEDGGKPLN
PPASTA**FPQE**PHGSPAAVNGNQPSFPPNSSGRGGTPDANSL
APPGKAGGGSGPQPPGLVYPCGACRSEVNDQDAILCEASCOK
WFHRECTGMTESAYGLLTTEASAVWACDLCLKTKEIQSVYIREGM
GQLVAANDG

FIG. 1

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ALIGNMENT OF HPYGO1 VS HPYGO2

VERSION BLASTP 2.2.6

Sequence 1 gi 19550449 pygopus 1 [Homo sapiens] Length 419 (1 .. 419)
 Sequence 2 gi 21594198 Pygopus 2 [Homo sapiens] Length 406 (1 .. 406)

Score = 240 bits (613)

Identities = 161/439 (36%)

Positives = 214/439 (48%)

Gaps = 58/439 (13%)

Pygo1: 3 AENSPAPAYKVSSHGGDSGLDG-----LGGPGVQLGSPDKKKRKANTQGPSFPPLSEY 55
 A ++P P K+ GG + G G+Q+ SP+KK+RK+NTQGP++ L+E+
 Pygo2: 2 AASAPPAPPDKLEGGGGPPAPPAPPSTGRKQGKAGLQMKSPEKKRRKSNTQGPAYSHLTER 61

Pygo1: 56 APPPNPNSDHHLVAANPFDDNYNTISYKPLPSSNPYLGPGYPGFGGYSTFR-MPPHVPPRM 114
 APPP P DHLVA+NPF+D++ + K ++ P+LG P FGG+ M VPP
 Pygo2: 62 APPPTPMVDHLVASNPFEDEDFG--APKVGVAAPPFLGSPVP-FGGFRVQGGMAGQVPPGY 118

Pygo1: 115 SSPYCG-PYSLRNQPHFPQNPQPLGMGFNRP-HAFNFGPHDNSSFGNPSYNNALSQNVNMP 172
 S+ G P LR QP PFP NP+G FN P + P N +F + +N L QN + P
 Pygo2: 119 STGGGGGPQPLRRQPPPFPNPMPGAFNMPQGPQYPPPGNMNFPQFNQPLGQNFSP 178

Pygo1: 173 NQHFRQNPAENFSQI-----PPQNASQVSNPDLASNFVPGNNNSNFTSPLESNHSFIP- 224
 + P F + PP+ +++ P L+ F SPL+ +P
 Pygo2: 179 SGQMMMPGPVGGFGPMISPTMGQPPR--AELGPPSLSQRFAQPGAPFGPSPLQRPGQGLPS 236

Pygo1: 225 -PPNTFGQAKAPPKQDFTQGATKNTQNSSAHPPHLNMDDTVNQSNIELKNVNRNNAVN 283
 PPNT +P P D + +PP + A
 Pygo2: 237 LPPNT-----SPFPGPDPGPFPGPQGEDGGKPLNPP-----ASTA AFP 272

Pygo1: 284 QENSRSSSTEATNNNPANGTQNKPQPRGAADACTTEKSNKSSLHPNRHGHSSDP--- 339
 QE S A N N + N + G DA + K+ G S P
 Pygo2: 273 QEPHSGSPAAVNGNQPSFPPNSSGRGGTPDANSLAPPKGAG-----GGSGPQPPPGL 326

Pygo1: 340 VYPCGICTNEVNDQDAILCEASCQKWFHRICTGMTEAYGLLTAEASAVWGCDTCMADK 399
 VYPCG C +EVNDDQDAILCEASCQKWFHR CTGMTE+AYGLLT EASAVW CD C+ K
 Pygo2: 327 VYPCGACRSEVNDQDAILCEASCQKWFHRECTGMTESAYGLLTTEASAVWACDLCLKTK 386

PHD-finger.
 PHD folds into an i>
 330 ****

Pygo1: 400 DVQLMRTRETFGPSAVGSD 418
 ++Q + RE G +D
 Pygo2: 387 EIQSIVIREGMGQLVAAND 405

FIG. 2

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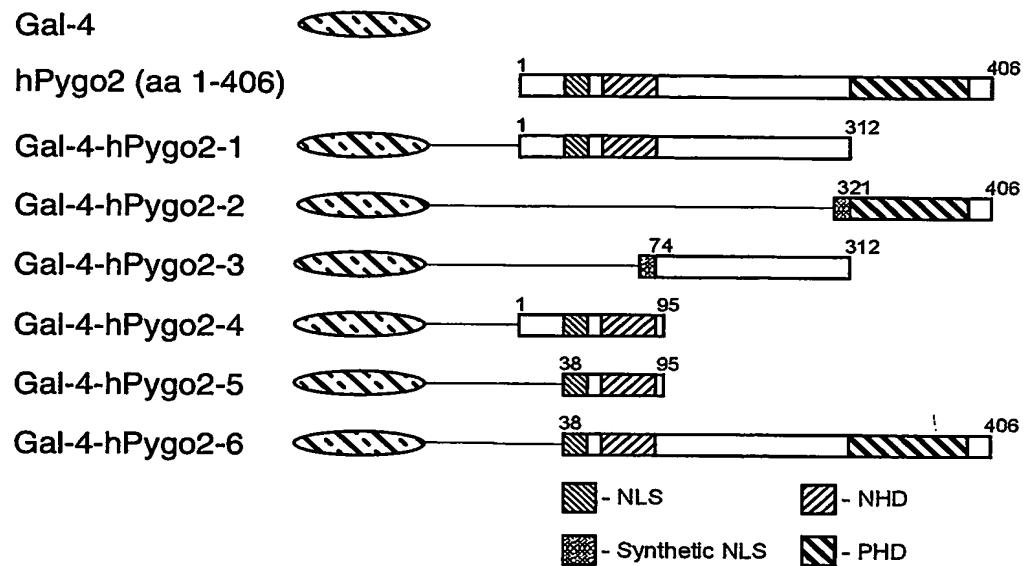


FIG. 3A

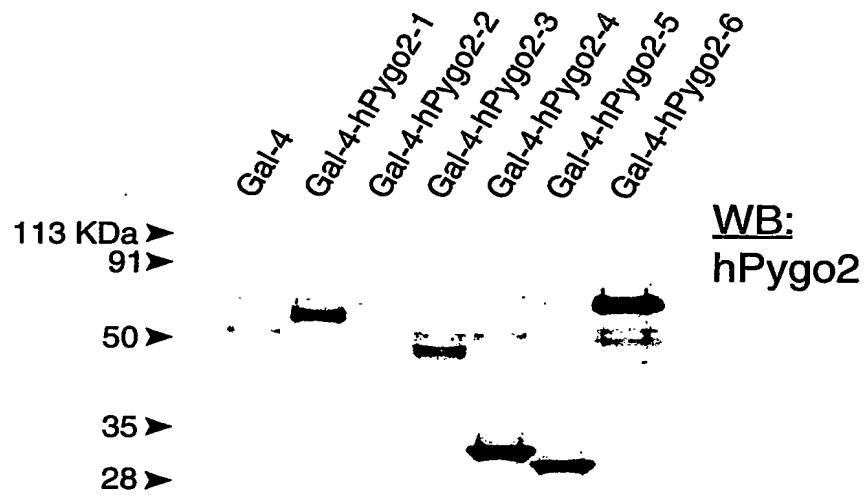


FIG. 3B

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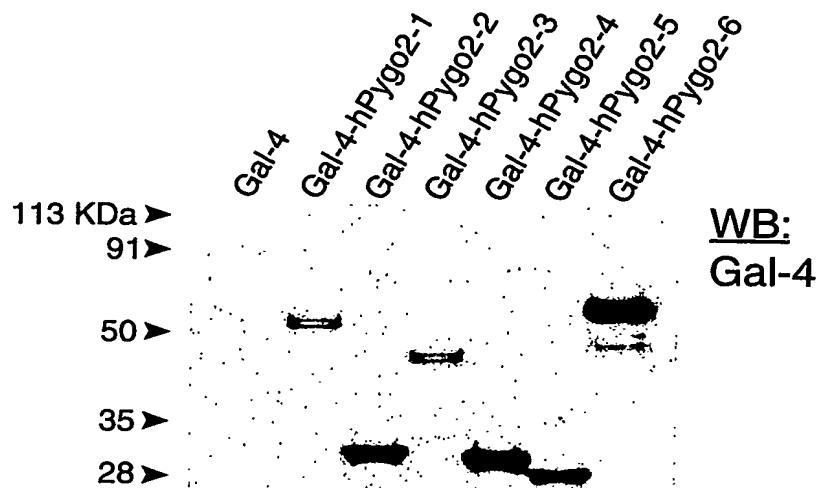


FIG. 3C

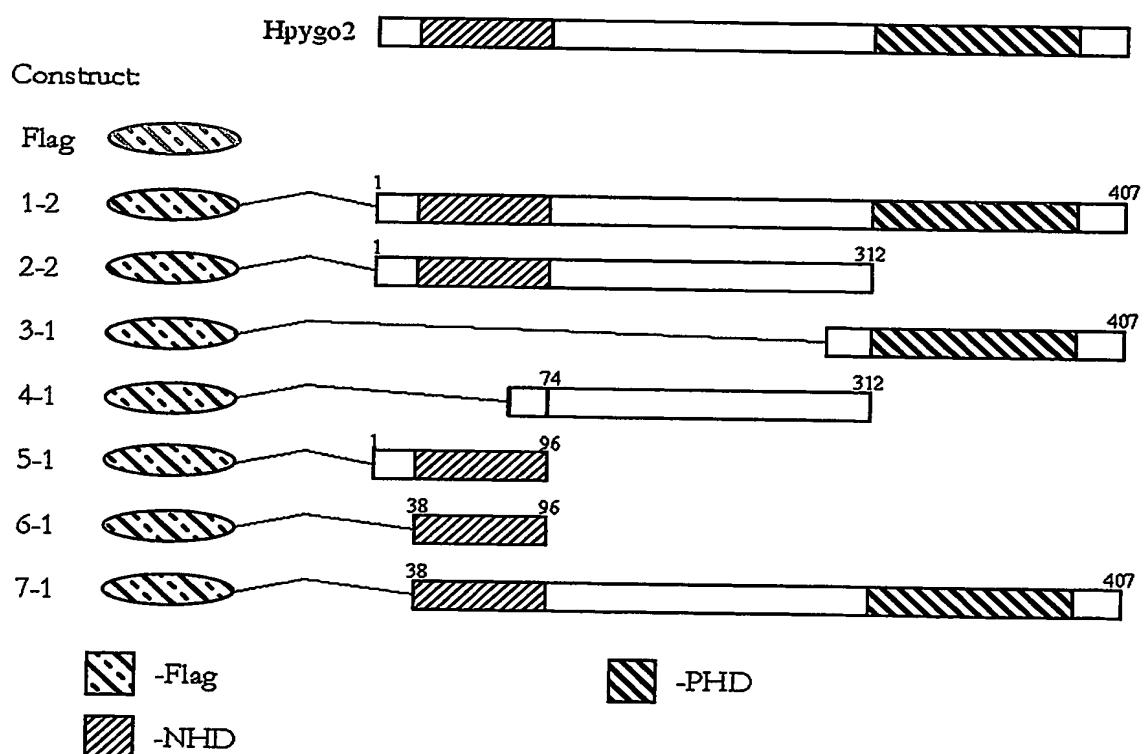


FIG. 3D

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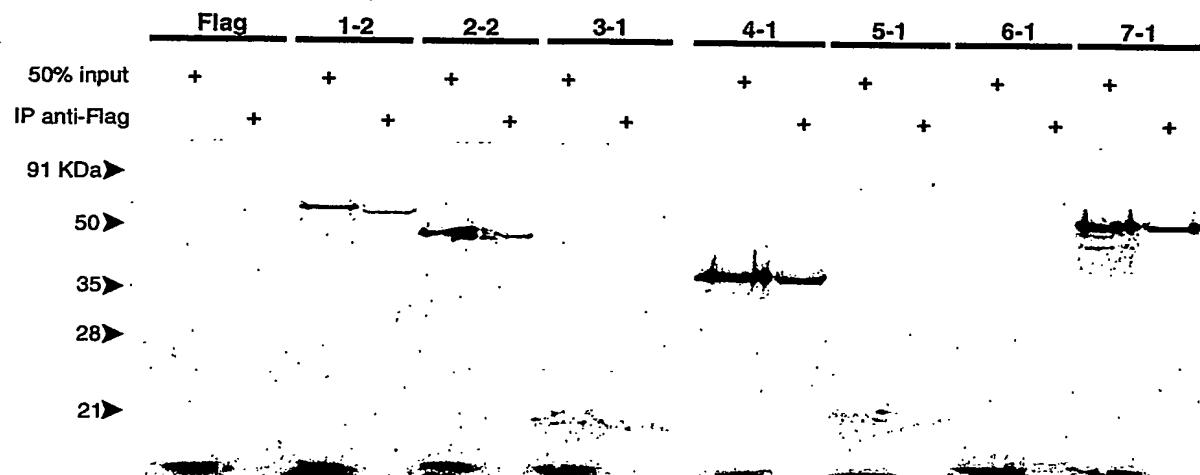


FIG. 3E

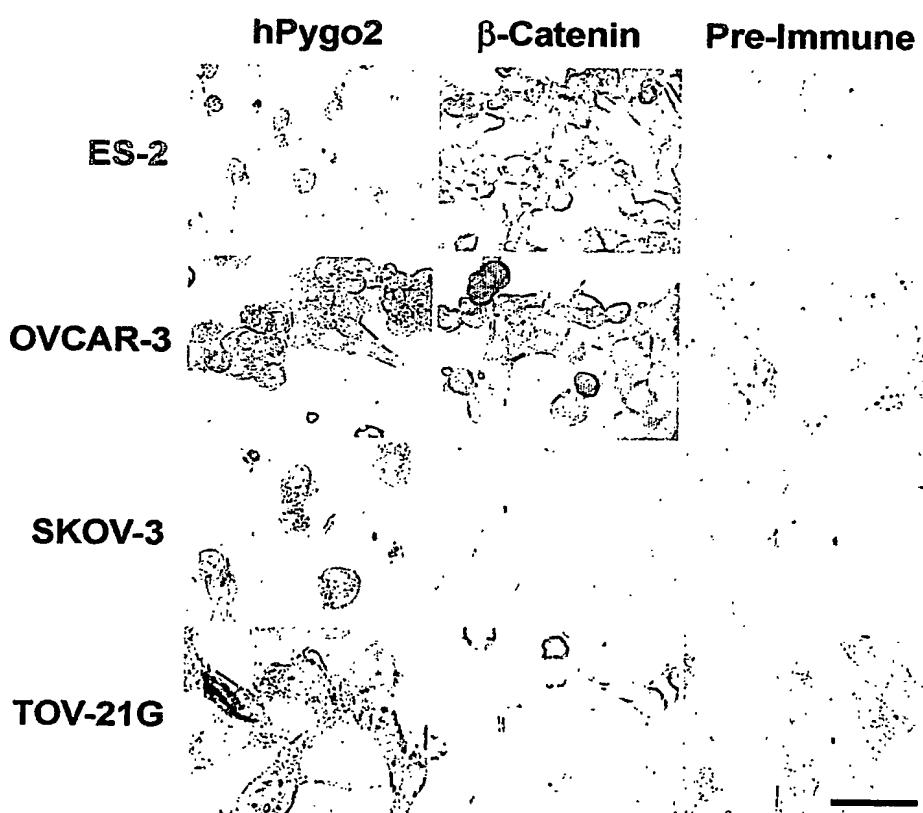


FIG. 3F

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hPygo2 cDNA

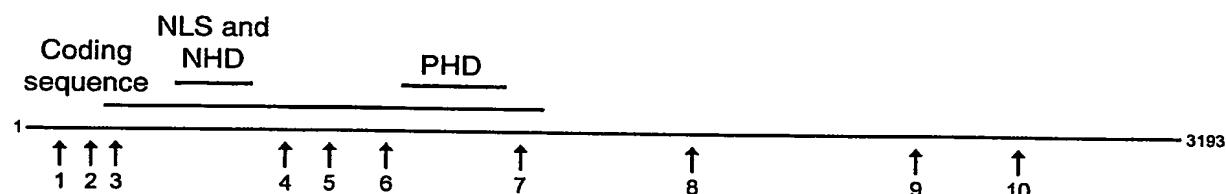


FIG. 3G

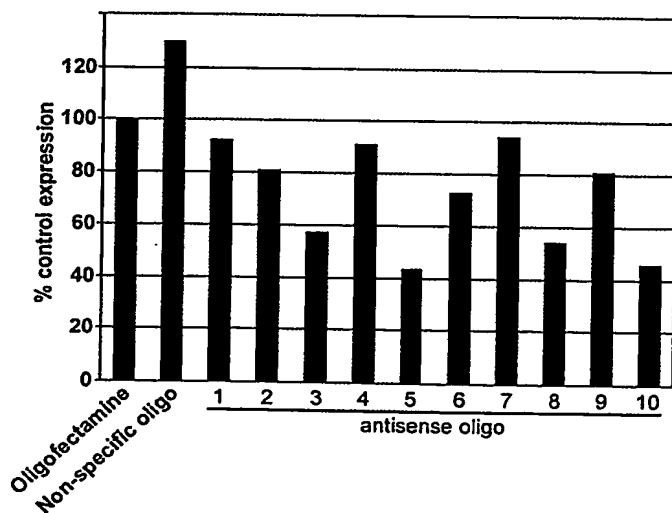
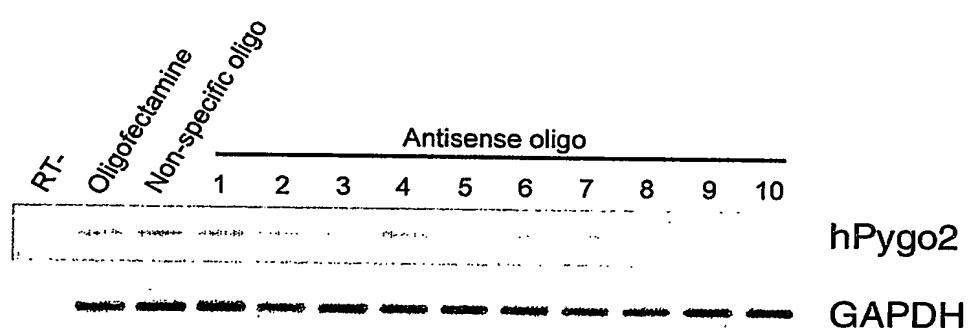


FIG. 3H

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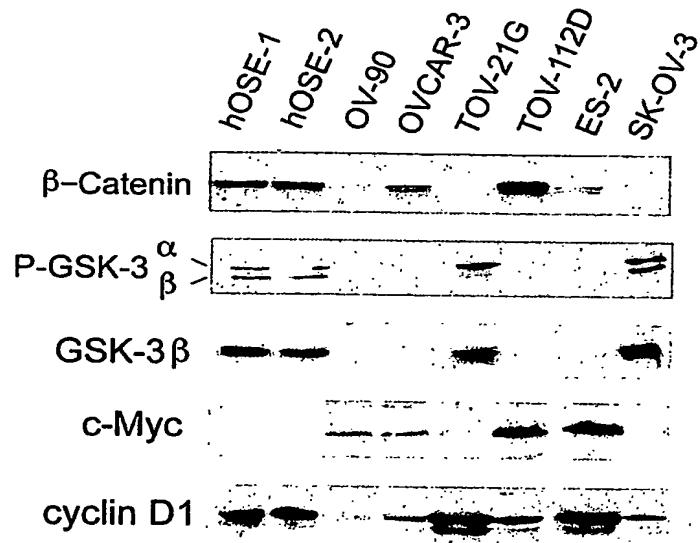


FIG. 4A

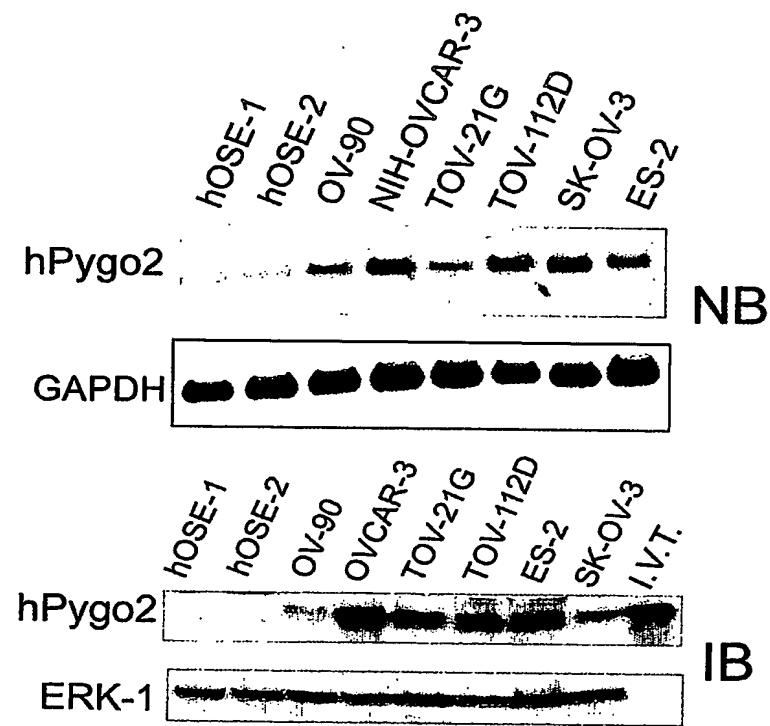


FIG. 4B

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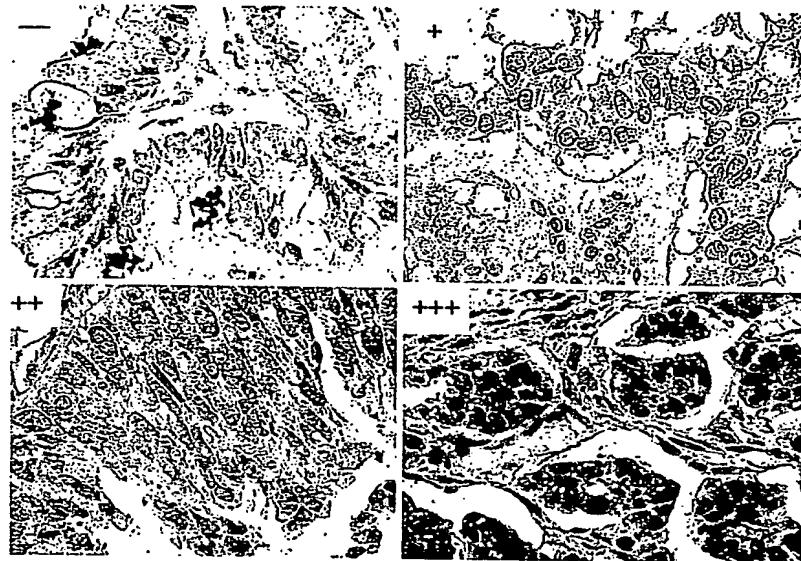


FIG. 4C

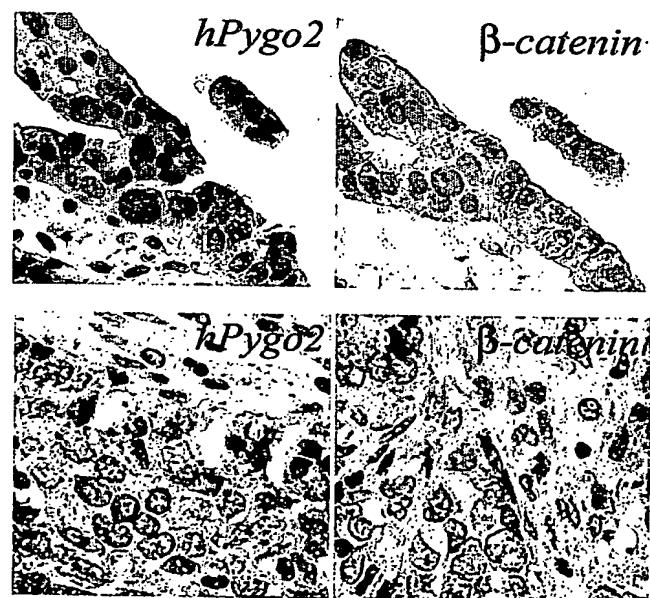


FIG. 4D

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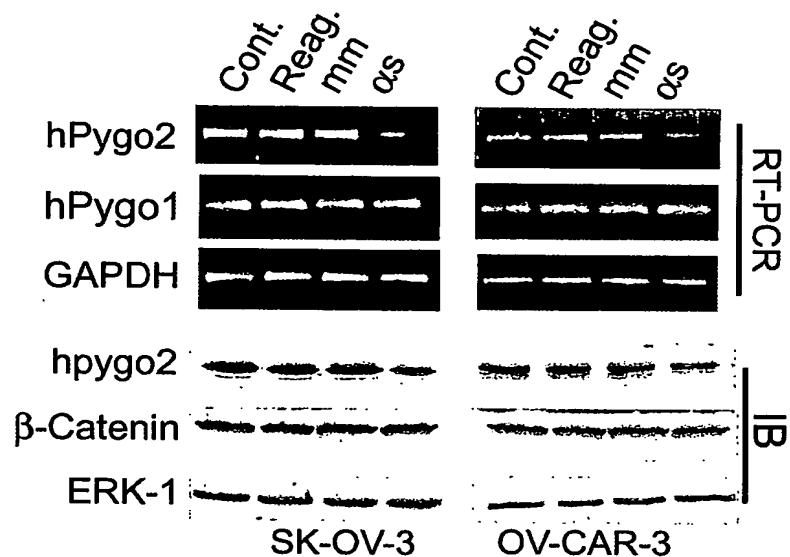


FIG. 5A

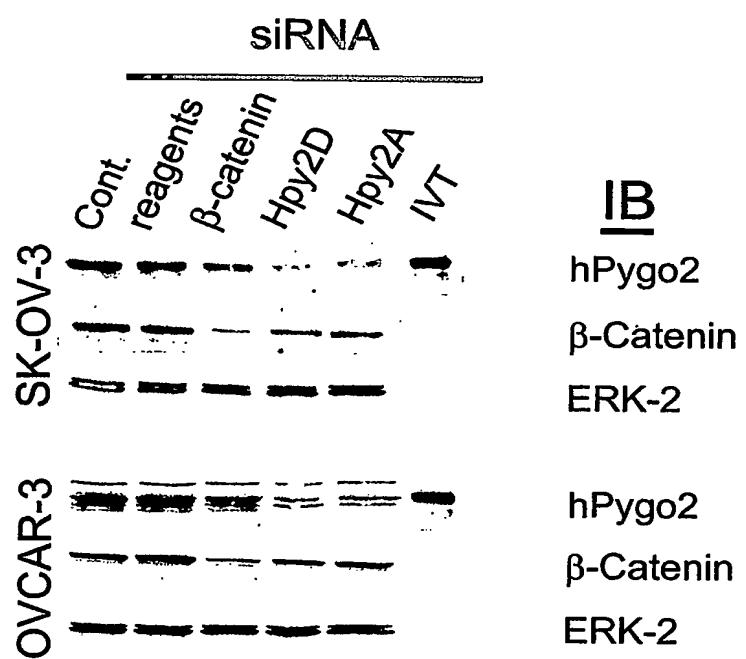
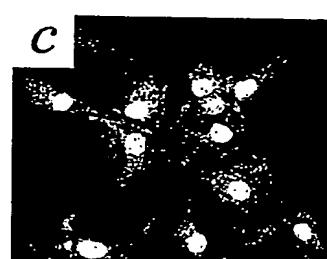
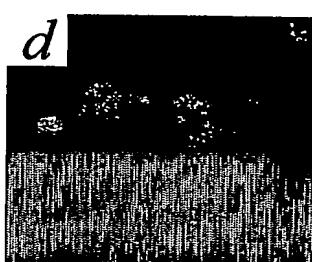
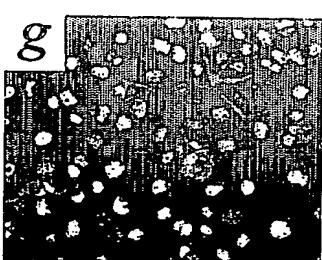


FIG. 5B

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**FIG. 6A****FIG. 6B****FIG. 6C****FIG. 6D****FIG. 6E****FIG. 6F****FIG. 6G****FIG. 6H****FIG. 6I****FIG. 6J****FIG. 6K****FIG. 6L**

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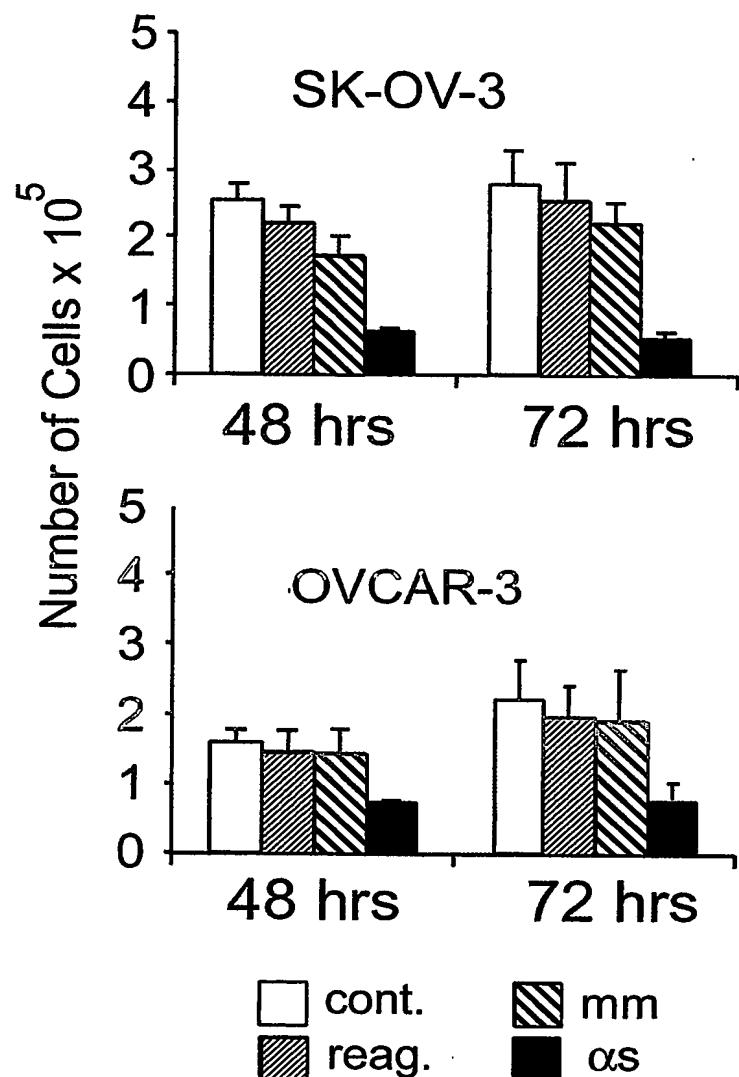


FIG. 7A

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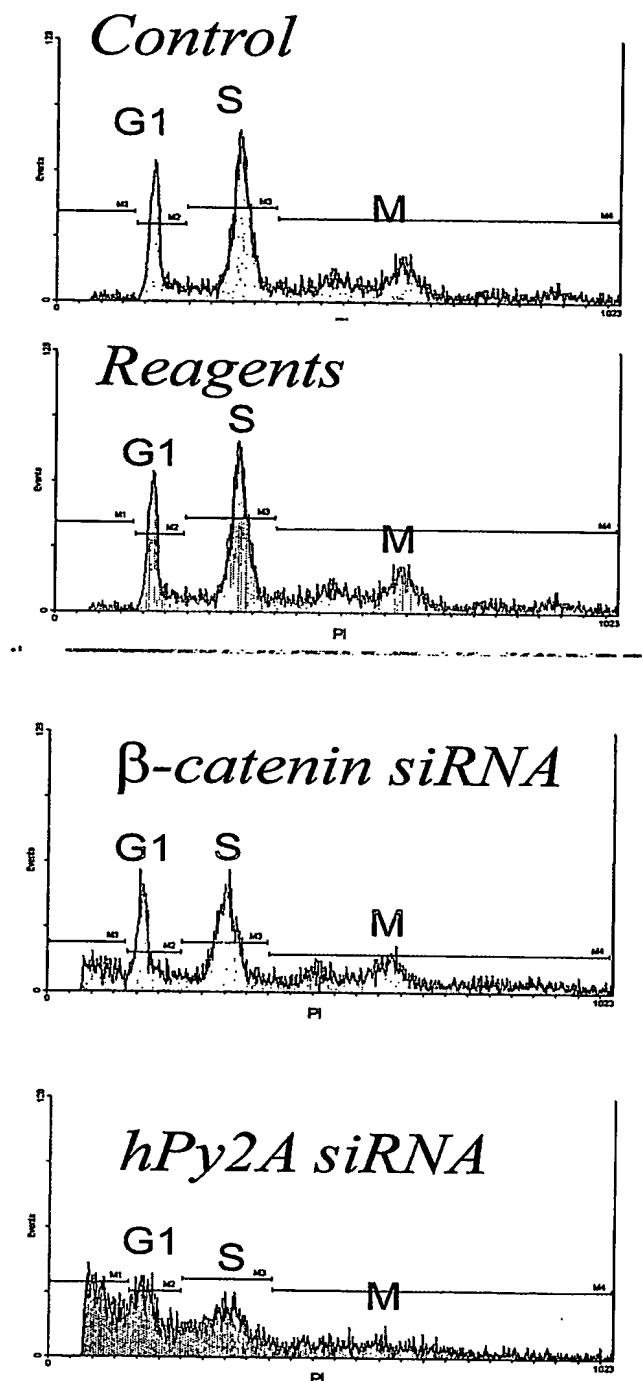


FIG. 7B

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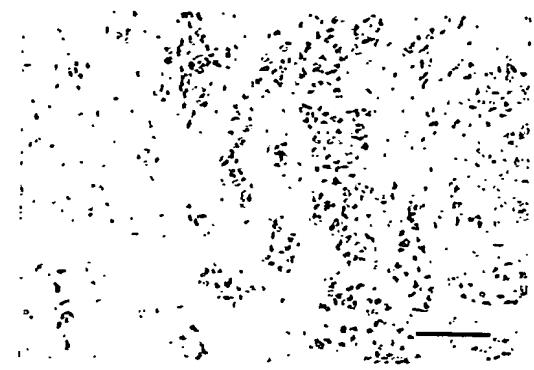


FIG. 8A



FIG. 8B

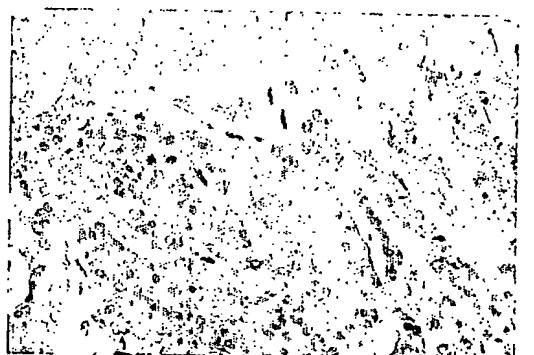


FIG. 8C

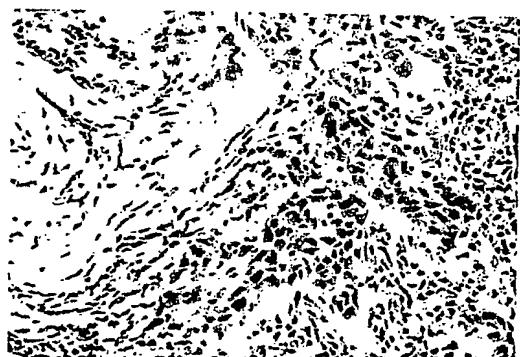


FIG. 8D

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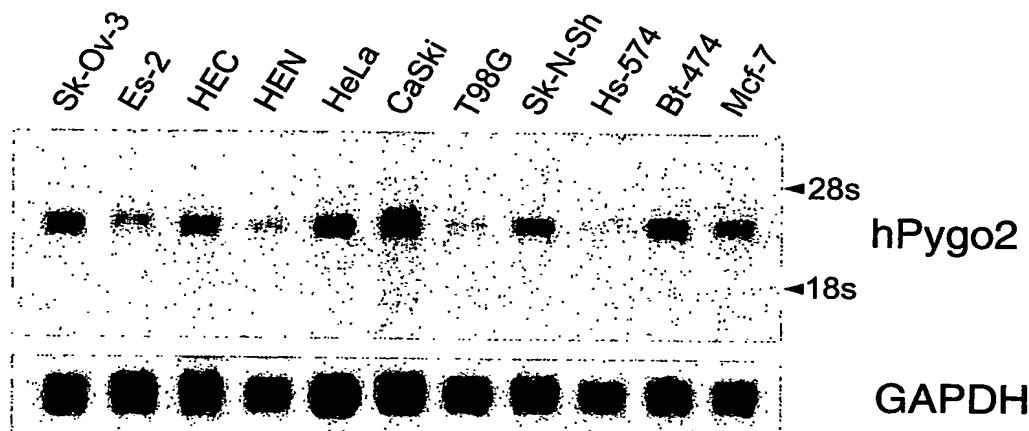


FIG. 9A

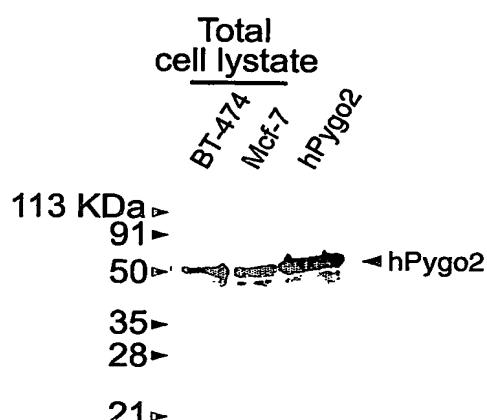


FIG. 9B

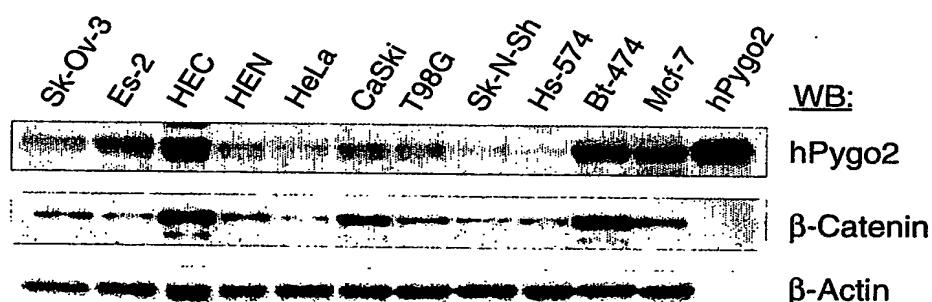


FIG. 9C

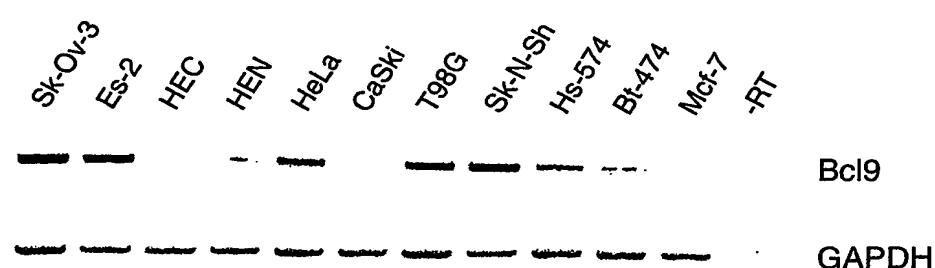


FIG. 9D

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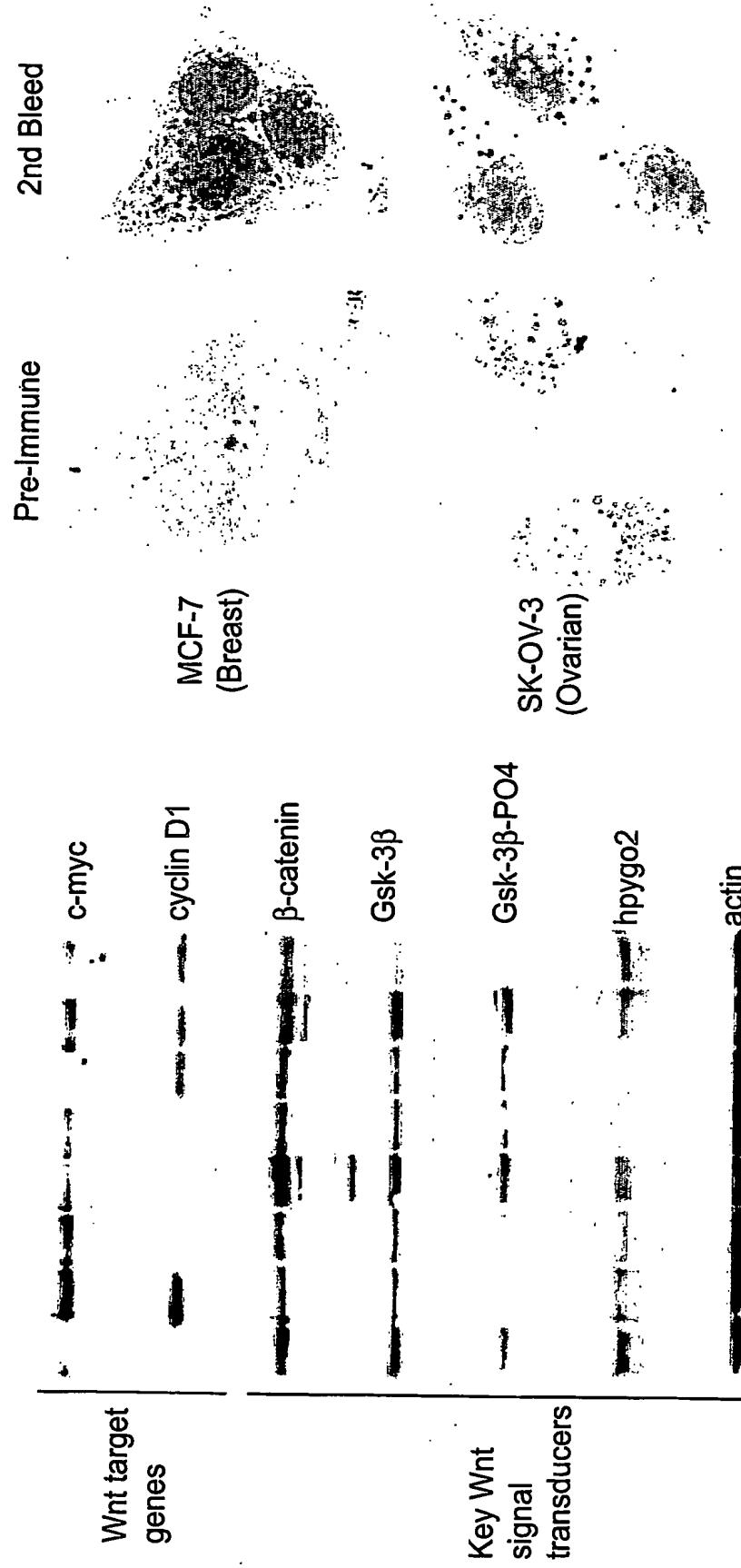


FIG. 9F

FIG. 9E

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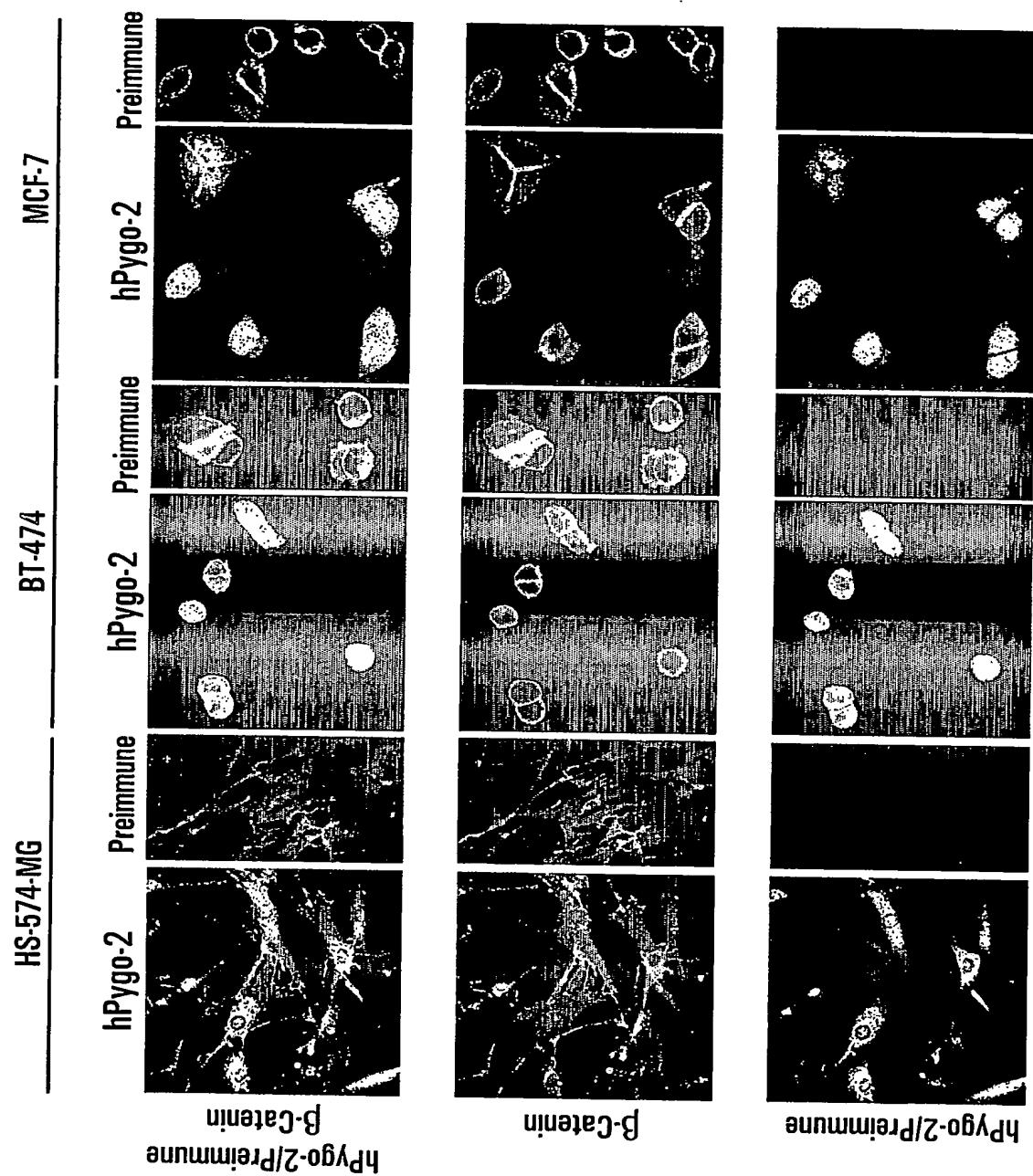


FIG. 10

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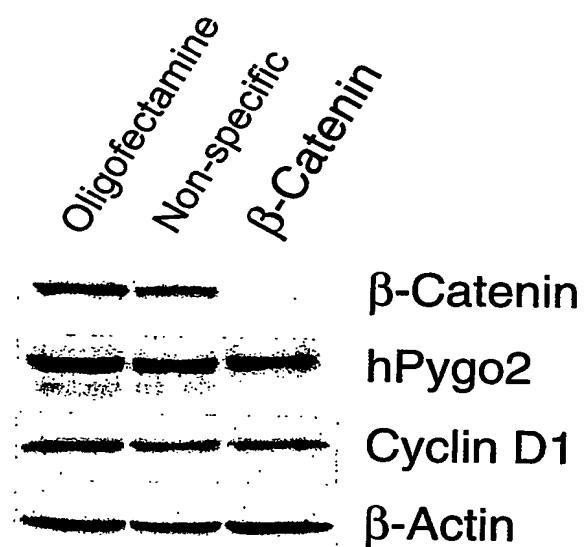


FIG. 11A

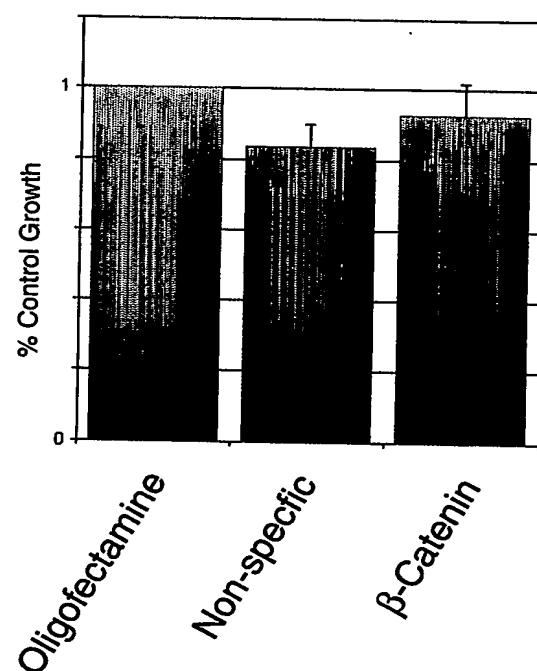
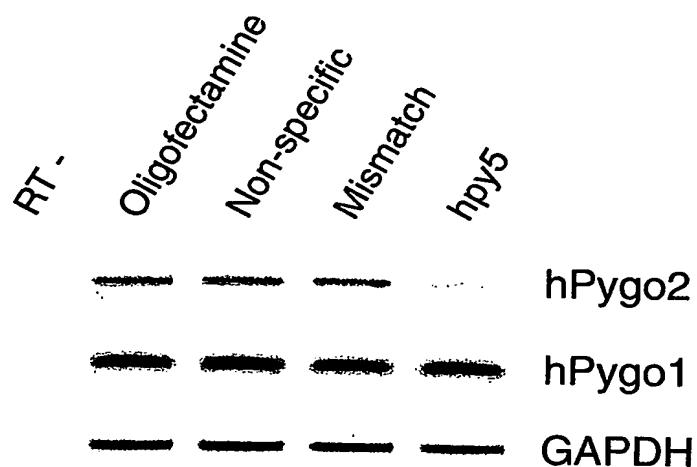
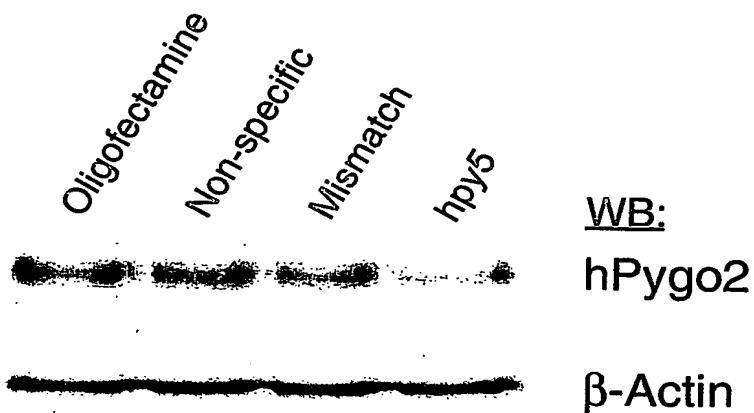
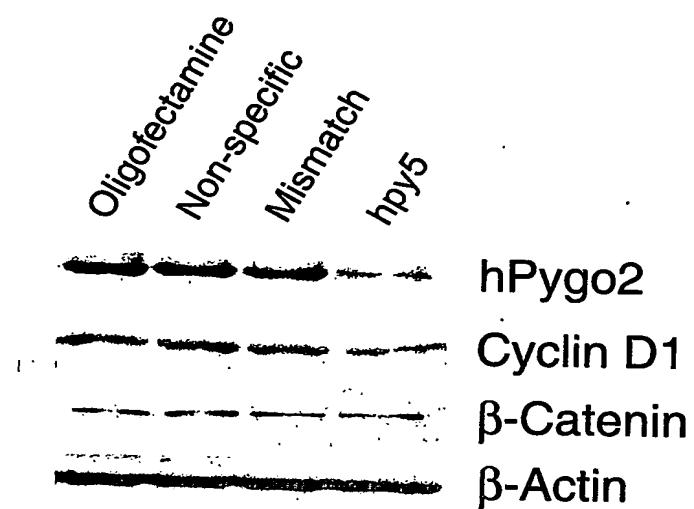
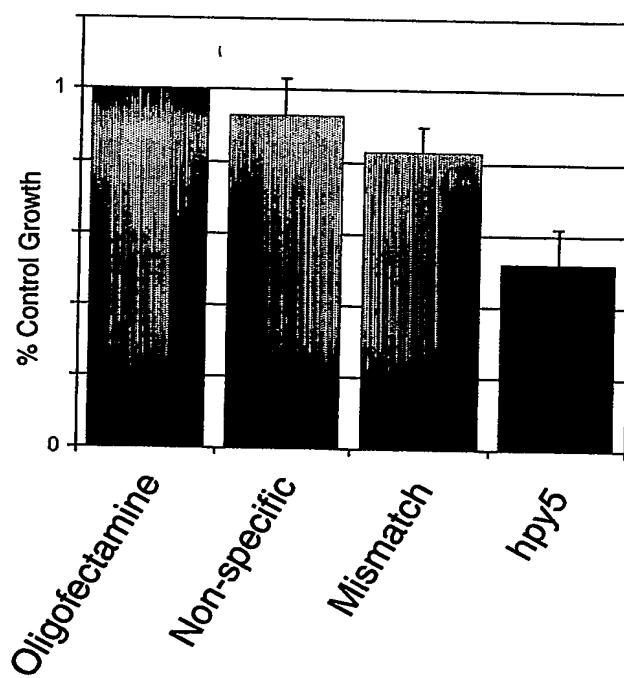


FIG. 11B

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FIG. 12A**FIG. 12B**

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**FIG. 13A****FIG. 13B**

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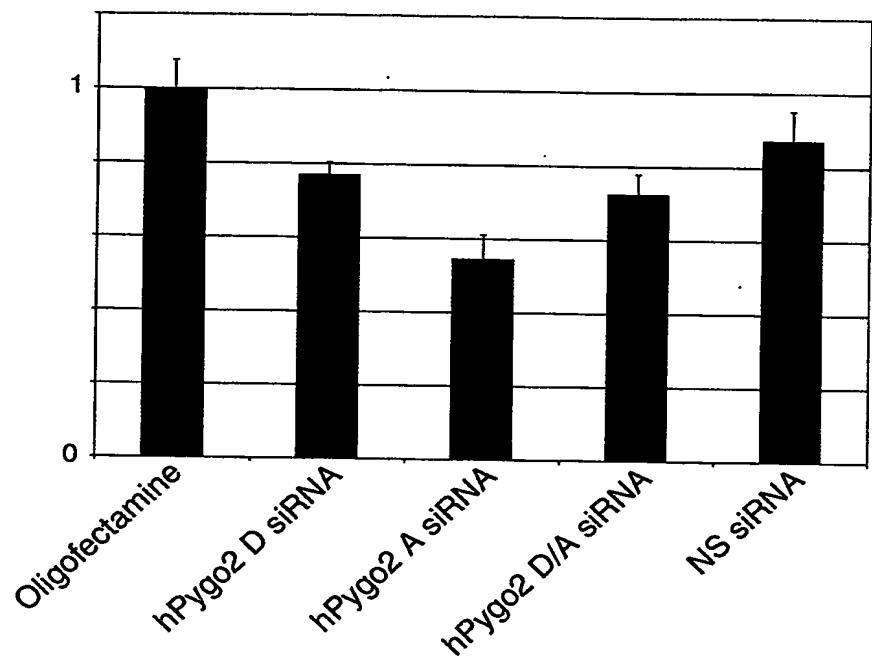


FIG. 14A

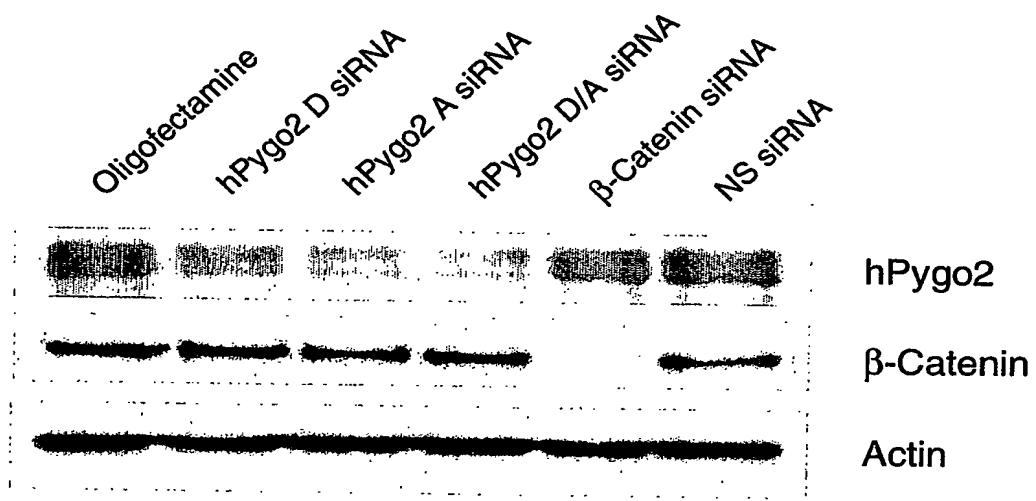
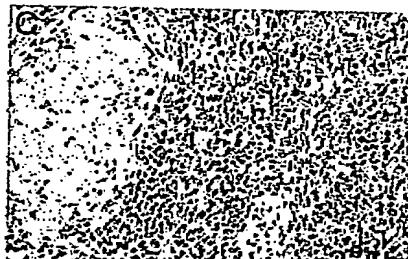
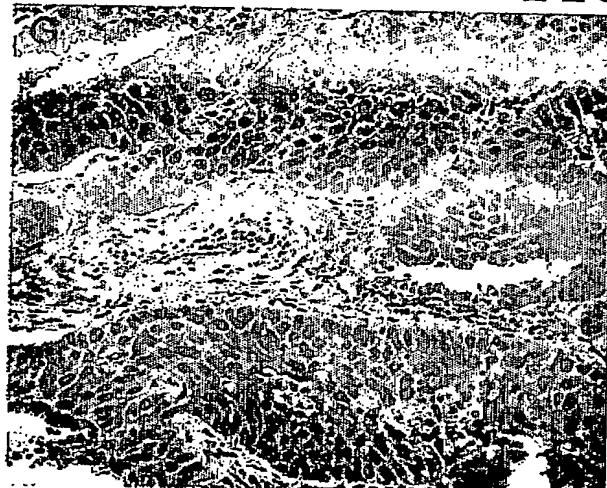
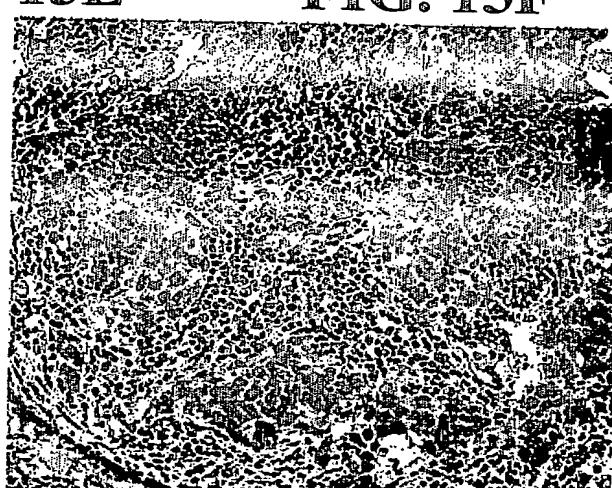
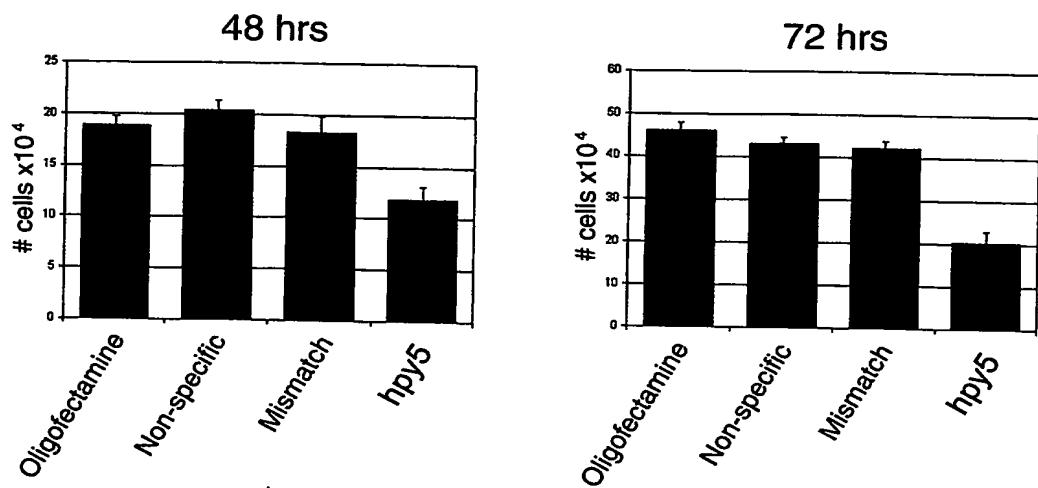
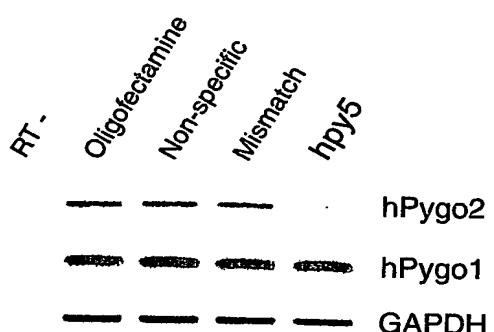
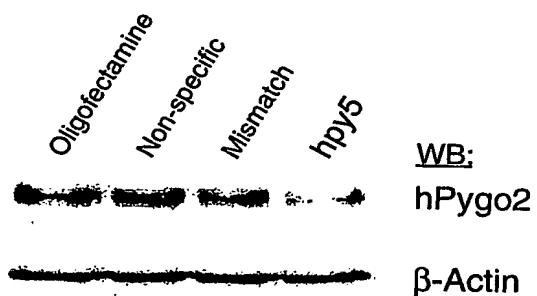


FIG. 14B

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**FIG. 15A****FIG. 15B****FIG. 15C****FIG. 15D****FIG. 15E****FIG. 15F****FIG. 15G****FIG. 15H**

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**FIG. 16A****FIG. 16B****FIG. 16C**